NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

[ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

[ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

[ ] 7. Other: _____

Applicant Must Provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
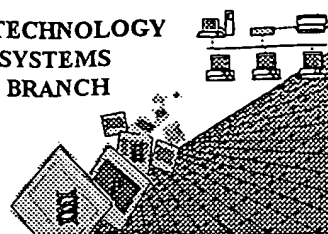PatentIn Software Program Support (SIRA)
    Technical Assistance...703-287-0200
    To Purchase PatentIn Software........................703-306-2600

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BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/612,925 β
Source: 1622
Date Processed by STIC: 7/24/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: 09/612,9258

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
      Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
      Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
      "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
      (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
      (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
      (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10_____Invalid <213>
      Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
      "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

1645

```
     RAW SEQUENCE LISTING                    DATE: 07/24/2002
     PATENT APPLICATION:   US/09/612,925B    TIME: 14:24:11

                 Input Set : A:\sequence listing.txt
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 3 <110> APPLICANT: Cano, Carlos Antonio Durante
 4         Nieto, Enrique Gerardo Guillen
 5         Acosta, Anabel Alvarez
 6         Munoz, Luis Emilio Carpio
 7         Vazquez, Diogenes Quintana
 8         Rodriguez, Carmen Elena Gomez Rodriguez
 9         Rodriguez, Recardo de la Caridad Siva
10         Galvez, Consuelo Nazabal
11         Angulo, Maria de Jesus Leal
12         Dunn, Alejandro Miguel Martin
14 <120> TITLE OF INVENTION: System for the Expression of Heterologous Antigens as Fusion
Proteins
16 <130> FILE REFERENCE: LEXSA P-13DIV2
18 <140> CURRENT APPLICATION NUMBER: 09/612,925B
19 <141> CURRENT FILING DATE: 2000-07-10
21 <150> PRIOR APPLICATION NUMBER: 08/930,917
22 <151> PRIOR FILING DATE: 1997-09-16
24 <150> PRIOR APPLICATION NUMBER: CU97/00001
25 <151> PRIOR FILING DATE: 1997-01-17
27 <160> NUMBER OF SEQ ID NOS: 21
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 47
33 <212> TYPE: PRT
34 <213> ORGANISM: Neisseria meningitidis
36 <400> SEQUENCE: 1
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42 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
43             20                  25                  30
46 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp
47          35                  40                  45
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 18
52 <212> TYPE: PRT
53 <213> ORGANISM: Neisseria meningitidis
55 <400> SEQUENCE: 2
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58 1               5                   10                  15
61 Ala Gly
65 <210> SEQ ID NO: 3
66 <211> LENGTH: 18
67 <212> TYPE: PRT
68 <213> ORGANISM: Neisseria meningitidis
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RAW SEQUENCE LISTING   DATE: 07/24/2002
PATENT APPLICATION: US/09/612,925B   TIME: 14:24:11

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Output Set: N:\CRF3\07242002\I612925B.raw

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76 Ala Ala
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83 <213> ORGANISM: Neisseria meningitidis
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88 1   5   10   15
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92   20   25
95 <210> SEQ ID NO: 5
96 <211> LENGTH: 146
97 <212> TYPE: PRT
98 <213> ORGANISM: Neisseria meningitidis
100 <400> SEQUENCE: 5
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103 1   5   10   15
106 Ala Gly Ala Ala Thr Gly Gly Cys Thr Thr Thr Ala Gly Thr Thr Gly
107   20   25   30
110 Ala Ala Thr Thr Gly Ala Ala Ala Gly Thr Gly Cys Cys Cys Gly Ala
111   35   40   45
114 Cys Ala Thr Thr Gly Gly Cys Gly Gly Ala Cys Ala Cys Gly Ala Ala
115   50   55   60
118 Ala Ala Thr Gly Thr Ala Gly Ala Thr Ala Thr Thr Ala Thr Cys Gly
119 65   70   75   80
122 Cys Gly Gly Thr Thr Gly Ala Ala Gly Thr Ala Ala Ala Cys Gly Thr
123   85   90   95
126 Gly Gly Gly Cys Gly Ala Cys Ala Cys Thr Ala Thr Thr Gly Cys Thr
127   100   105   110
130 Gly Thr Gly Gly Ala Cys Gly Ala Thr Ala Cys Cys Cys Thr Gly Ala
131   115   120   125
134 Thr Thr Ala Cys Thr Thr Thr Gly Gly Ala Thr Cys Thr Ala Gly Ala
135   130   135   140
138 Ala Ala
139 145
142 <210> SEQ ID NO: 6
143 <211> LENGTH: 47
144 <212> TYPE: PRT
145 <213> ORGANISM: Neisseria meningitidis
147 <400> SEQUENCE: 6
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150 1   5   10   15
153 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
154   20   25   30
157 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu
158   35   40   45

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163 <212> TYPE: PRT
164 <213> ORGANISM: Neisseria meningitidis
166 <400> SEQUENCE: 7
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169 1               5                   10                  15
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173 <211> LENGTH: 16
174 <212> TYPE: PRT
175 <213> ORGANISM: Neisseria meningitidis
177 <400> SEQUENCE: 8
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185 <212> TYPE: PRT
186 <213> ORGANISM: Human immunodeficiency virus type 1
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195 <211> LENGTH: 15
196 <212> TYPE: PRT
197 <213> ORGANISM: Human immunodeficiency virus type 1
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206 <211> LENGTH: 15
207 <212> TYPE: PRT
208 <213> ORGANISM: Human immunodeficiency virus type 1
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216 <210> SEQ ID NO: 12
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218 <212> TYPE: PRT
219 <213> ORGANISM: Human immunodeficiency virus type 1
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224 1               5                   10                  15
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229 <212> TYPE: PRT
230 <213> ORGANISM: Human immunodeficiency virus type 1
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235 1               5                   10                  15
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RAW SEQUENCE LISTING   DATE: 07/24/2002
PATENT APPLICATION: US/09/612,925B   TIME: 14:24:11

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240 <212> TYPE: PRT
241 <213> ORGANISM: Human immunodeficiency virus type 1
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246 1   5   10   15
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250 <211> LENGTH: 15
251 <212> TYPE: PRT
252 <213> ORGANISM: Human immunodeficiency virus type 1
254 <400> SEQUENCE: 15
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257 1   5   10   15
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261 <211> LENGTH: 15
262 <212> TYPE: PRT
263 <213> ORGANISM: Human immunodeficiency virus type 1
265 <400> SEQUENCE: 16
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271 <210> SEQ ID NO: 17
272 <211> LENGTH: 5
273 <212> TYPE: PRT
274 <213> ORGANISM: unidentified
276 <400> SEQUENCE: 17
278 Ala Gly Gly Gly Ala
279 1   5
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283 <211> LENGTH: 141
284 <212> TYPE: PRT
285 <213> ORGANISM: Human immunodeficiency virus type 1
287 <400> SEQUENCE: 18
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293 His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile
294   20   25   30
297 Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Gly Ala Arg Gln
298   35   40   45
301 Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr Thr Thr Ala Gly Gly
302   50   55   60
305 Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala
306 65   70   75   80
309 Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg
310   85   90   95
313 Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile Thr Met
314   100   105   110
317 Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Gly Ala Ser Ile
318   115   120   125

RAW SEQUENCE LISTING   DATE: 07/24/2002
PATENT APPLICATION: US/09/612,925B   TIME: 14:24:11

Input Set : A:\sequence listing.txt
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322     130             135             140
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326 <211> LENGTH: 162
327 <212> TYPE: PRT
328 <213> ORGANISM: Human immunodeficiency virus type 1
330 <400> SEQUENCE: 19
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333 1               5                   10                  15
336 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
337             20              25                  30
340 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser
341         35              40                  45
344 Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly
345     50              55                  60
348 Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr
349 65                  70                  75                  80
352 Thr Thr Ala Gly Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly
353             85                  90                  95
356 Arg Val Ile Tyr Ala Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His
357             100                 105                 110
360 Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg
361             115                 120                 125
364 Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly
365     130             135                 140
368 Gly Gly Ala Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val
369 145                 150                 155                 160
372 Thr Ile
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377 <211> LENGTH: 202
378 <212> TYPE: PRT
379 <213> ORGANISM: Human immunodeficiency virus type 1
381 <400> SEQUENCE: 20
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387 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
388             20              25                  30
391 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser
392         35              40                  45
395 Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly
396     50              55                  60
399 Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr
400 65                  70                  75                  80
403 Thr Thr Ala Gly Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly
404             85                  90                  95
407 Arg Val Ile Tyr Ala Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His
408             100                 105                 110
411 Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg
412             115                 120                 125
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VERIFICATION SUMMARY   DATE: 07/24/2002
PATENT APPLICATION: US/09/612,925B   TIME: 14:24:12

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